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SEQUENCE LISTING

<110> Liao et al.

<120> ALANINE 2,3-AMINOMUTASE

<130> 63358-09

<150> PCT/US03/01635

<151> 2003-01-17

<150> US 60/350,727

<151> 2002-01-18

<150> US 60/375,785

<151> 2002-04-25

<160> 66

<170> PatentIn version 3.1

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<213> Artificial Sequence

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36

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<211> 1416

<212> DNA

<213> Bacillus subtilis

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120

gatgattaa agaaagtcat taatctgacc gaggatgaag aggaaggcgt cagaatttct	180
acccaaaacga tccccttaaa tattacacct tactatgctt cttaatgga ccccgacaat	240
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gatcggcgtg agaaaagaga tcagctaaa gaaaagaaaat ttttggcgca gcagaaaaaa	1380
cagaaagaga ctgaatgcgg aggggattct tcatga	1416

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<223> PCR primer

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<221> misc_feature

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23

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> misc_feature

<222> (1)..(20)

<223> y is t/u or c; s is g or c; b is g, c or t/u; w is a or t/u; n is a, c, g or t/u.

<400> 17

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20

<210> 18

<211> 21

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<212> DNA
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<222> (1)..(21)
<223> y is t/u or c; r is g or a; n is a, c, g or t/u.

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<212> DNA
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ggtttacgag ggcgagaacg gcttgct 27

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<211> 1416
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<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1416)
<223>

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1 5 10 15

tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96
Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
20 25 30

ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144
Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
35 40 45

ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192
Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
50 55 60

ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240

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Pro	Arg	Cys	Pro	Val	Arg	Met	Gln	Ser	Val	Pro	Leu	Ser	Glu	Glu	Met	
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cac aaa aca aaa tac gat atg gaa gac ccg ctt cat gag gat gaa gat															336	
His	Lys	Thr	Lys	Tyr	Asp	Met	Glu	Asp	Pro	Leu	His	Glu	Asp	Glu	Asp	
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Ser	Pro	Val	Pro	Gly	Leu	Thr	His	Arg	Tyr	Pro	Asp	Arg	Val	Leu	Phe	
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Leu	Val	Thr	Asn	Gln	Cys	Ser	Val	Tyr	Cys	Arg	Tyr	Cys	Thr	Arg	Arg	
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Arg	Phe	Ser	Gly	Gln	Ile	Gly	Met	Gly	Val	Pro	Lys	Lys	Gln	Leu	Asp	
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gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta															528	
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					165				170			175				
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Ile	Ser	Gly	Gly	Asp	Gly	Leu	Leu	Ile	Asn	Asp	Gln	Ile	Leu	Glu	Tyr	
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att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc aga atc															624	
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tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt															720	
Cys	Glu	Ile	Leu	Lys	Lys	Tyr	His	Pro	Val	Trp	Leu	Asn	Thr	His	Phe	
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aac aca agc atc gaa atg aca gaa tcc gtt gag gca tgt gaa aag															768	
Asn	Thr	Ser	Ile	Glu	Met	Thr	Glu	Glu	Ser	Val	Glu	Ala	Cys	Glu	Lys	
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Leu	Val	Asn	Ala	Gly	Val	Pro	Val	Gly	Asn	Gln	Ala	Val	Val	Leu	Ala	
					260				265			270				
ggt att aat gat tcg gtt cca att atg aaa aag ctc atg cat gac ttg															864	
Gly	Ile	Asn	Asp	Ser	Val	Pro	Ile	Met	Lys	Lys	Leu	Met	His	Asp	Leu	
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290

295

300

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gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe 405 410 415	1248
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aat ccg gag cat gaa aca tta aaa gat ccg cgt gag aaa aga gat cag Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln 435 440 445	1344
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr 450 455 460	1392
gaa tgc gga ggg gat tct tca tga Glu Cys Gly Gly Asp Ser Ser 465 470	1416

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 <212> PRT
 <213> *Bacillus subtilis*

<400> 21

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Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
35 40 45

Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
85 90 95

His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp
100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
115 120 125

Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg
130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
325 330 335

Val Val His Ala Pro Gly Gly Lys Ile Ala Leu Gln Pro Asn
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
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Glu Cys Gly Gly Asp Ser Ser

465

470

<210> 22
<211> 438
<212> DNA
<213> Clostridium propionicum

<220>
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<222> (1)..(438)
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1 5 10 15

gct cac tat act gga aac tta gta aac ggc gct aga att gtg aat cag 96
Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln
20 25 30

tgg ggc gac gtt ggt aca gaa tta atg gtt tat gtt gat ggt gac ata 144
Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
35 40 45

agc tta ttc ttg ggc tac aaa gat atc gaa ttc aca gct cct gta tat 192
Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr
50 55 60

gtt ggt gac ttt atg gaa tac cac ggc tgg att gaa aaa gtt ggt aac 240
Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn
65 70 75 80

cag tcc tat aca tgt aaa ttt gaa gca tgg aaa gtt gca aca atg gtt 288
Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Thr Met Val
85 90 95

gat atc aca aat cct cag gat aca cgc gca aca gct tgt gag cct ccg 336
Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro
100 105 110

gta ttg tgc gga aga gca acg ggt agt ttg ttc atc gca aaa aaa gat 384
Val Leu Cys Gly Arg Ala Thr Gly Ser Leu Phe Ile Ala Lys Lys Asp
115 120 125

cag aga ggc cct cag gaa tcc tct ttt aaa gag aga aag cac ccc ggt 432
Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Glu Arg Lys His Pro Gly
130 135 140

gaa tga 438
Glu
145

<210> 23

<211> 145

<212> PRT

<213> Clostridium propionicum

<400> 23

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20 25 30

Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
35 40 45

Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr
50 55 60

Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn
65 70 75 80

Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Thr Met Val
85 90 95

Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro
100 105 110

Val Leu Cys Gly Arg Ala Thr Gly Ser Leu Phe Ile Ala Lys Lys Asp
115 120 125

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Glu

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<210> 24

<211> 1554

<212> DNA

<213> Megasphaera elsdenii

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<222> (1)..(1554)

<223>

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aaa gac aac gac acg att acg tct atc ggc ttt gtc agc agc gcc cat	96
Lys Asp Asn Asp Thr Ile Thr Ser Ile Gly Phe Val Ser Ser Ala His	
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ccg gaa gca ctg acc aaa gct ttg gaa aaa cgg ttc ctg gac acg aac	144
Pro Glu Ala Leu Thr Lys Ala Leu Glu Lys Arg Phe Leu Asp Thr Asn	
35 40 45	
acc ccg cag aac ttg acc tac atc tat gca ggc tct cag ggc aaa cgc	192
Thr Pro Gln Asn Leu Thr Tyr Ile Tyr Ala Gly Ser Gln Gly Lys Arg	
50 55 60	
gat ggc cgt gcc gct gaa cat ctg gca cac aca ggc ctt ttg aaa cgc	240
Asp Gly Arg Ala Ala Glu His Leu Ala His Thr Gly Leu Leu Lys Arg	
65 70 75 80	
gcc atc atc ggt cac tgg cag act gta ccg gct atc ggt aaa ctg gct	288
Ala Ile Ile Gly His Trp Gln Thr Val Pro Ala Ile Gly Lys Leu Ala	
85 90 95	
gtc gaa aac aag att gaa gct tac aac ttc tcg cag ggc acg ttg gtc	336
Val Glu Asn Lys Ile Glu Ala Tyr Asn Phe Ser Gln Gly Thr Leu Val	
100 105 110	
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His Trp Phe Arg Ala Leu Ala Gly His Lys Leu Gly Val Phe Thr Asp	
115 120 125	
atc ggt ctg gaa act ttc ctc gat ccc cgt cag ctc ggc ggc aag ctc	432
Ile Gly Leu Glu Thr Phe Leu Asp Pro Arg Gln Leu Gly Gly Lys Leu	
130 135 140	
aat gac gta acc aaa gaa gac ctc gtc aaa ctg atc gaa gtc gat ggt	480
Asn Asp Val Thr Lys Glu Asp Leu Val Lys Leu Ile Glu Val Asp Gly	
145 150 155 160	
cat gaa cag ctt ttc tac ccg acc ttc ccg gtc aac gta gct ttc ctc	528
His Glu Gln Leu Phe Tyr Pro Thr Phe Pro Val Asn Val Ala Phe Leu	
165 170 175	
cgc ggt acg tat gct gat gaa tcc ggc aat atc acc atg gac gaa gaa	576
Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Met Asp Glu Glu	
180 185 190	
atc ggg cct ttc gaa agc act tcc gta gcc cag gcc gtt cac aac tgt	624
Ile Gly Pro Phe Glu Ser Thr Ser Val Ala Gln Ala Val His Asn Cys	
195 200 205	
ggc ggt aaa gtc gtc gtc cag gtc aaa gac gtc gtc gct cac ggc agc	672
Gly Gly Lys Val Val Val Gln Val Lys Asp Val Val Ala His Gly Ser	
210 215 220	

ctc gac ccg cgc atg gtc aag atc cct ggc atc tat gtc gac tac gtc Leu Asp Pro Arg Met Val Lys Ile Pro Gly Ile Tyr Val Asp Tyr Val 225 230 235 240	720
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gca gct ctc ccc atg agc gct aag aaa atc atc ggc cgc cgc ggc gct Ala Ala Leu Pro Met Ser Ala Lys Lys Ile Ile Gly Arg Arg Gly Ala 275 280 285	864
ttg gaa ttg act gaa aac gct gtc gtc aac ctc ggc gtc ggt gct ccg Leu Glu Leu Thr Glu Asn Ala Val Val Asn Leu Gly Val Gly Ala Pro 290 295 300	912
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aca ccg aat gtt tac ttc tgc ggc acc ttc acg gct ggc ggc ttg aaa Thr Pro Asn Val Tyr Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys 405 410 415	1248
atc gct gtc gaa gac ggc aaa gtc aag atc ctc cag gaa ggc aaa gcc Ile Ala Val Glu Asp Gly Lys Val Lys Ile Leu Gln Glu Gly Lys Ala 420 425 430	1296
aag aag ttc atc aaa gct gtc gac cag atc act ttc aac ggt tcc tat Lys Lys Phe Ile Lys Ala Val Asp Gln Ile Thr Phe Asn Gly Ser Tyr 435 440 445	1344
gca gcc cgc aac ggc aaa cac gtt ctc tac atc aca gaa cgc tgc gta	1392

Ala Ala Arg Asn Gly Lys His Val Leu Tyr Ile Thr Glu Arg Cys Val			
450	455	460	
ttt gaa ctg acc aaa gaa ggc ttg aaa ctc atc gaa gtc gca ccg ggc			1440
Phe Glu Leu Thr Lys Glu Gly Leu Lys Leu Ile Glu Val Ala Pro Gly			
465	470	475	480
atc gat att gaa aaa gat atc ctc gct cac atg gac ttc aag ccg atc			1488
Ile Asp Ile Glu Lys Asp Ile Leu Ala His Met Asp Phe Lys Pro Ile			
485	490	495	
att gat aat ccg aaa ctc atg gat gcc cgc ctc ttc cag gac ggt ccc			1536
Ile Asp Asn Pro Lys Leu Met Asp Ala Arg Leu Phe Gln Asp Gly Pro			
500	505	510	
atg gga ctg aaa aaa taa			1554
Met Gly Leu Lys Lys			
515			
<210> 25			
<211> 517			
<212> PRT			
<213> Megasphaera elsdenii			
<400> 25			
Met Arg Lys Val Glu Ile Ile Thr Ala Glu Gln Ala Ala Gln Leu Val			
1	5	10	15
Lys Asp Asn Asp Thr Ile Thr Ser Ile Gly Phe Val Ser Ser Ala His			
20	25	30	
Pro Glu Ala Leu Thr Lys Ala Leu Glu Lys Arg Phe Leu Asp Thr Asn			
35	40	45	
Thr Pro Gln Asn Leu Thr Tyr Ile Tyr Ala Gly Ser Gln Gly Lys Arg			
50	55	60	
Asp Gly Arg Ala Ala Glu His Leu Ala His Thr Gly Leu Leu Lys Arg			
65	70	75	80
Ala Ile Ile Gly His Trp Gln Thr Val Pro Ala Ile Gly Lys Leu Ala			
85	90	95	
Val Glu Asn Lys Ile Glu Ala Tyr Asn Phe Ser Gln Gly Thr Leu Val			
100	105	110	
His Trp Phe Arg Ala Leu Ala Gly His Lys Leu Gly Val Phe Thr Asp			
115	120	125	

Ile Gly Leu Glu Thr Phe Leu Asp Pro Arg Gln Leu Gly Gly Lys Leu
130 135 140

Asn Asp Val Thr Lys Glu Asp Leu Val Lys Leu Ile Glu Val Asp Gly
145 150 155 160

His Glu Gln Leu Phe Tyr Pro Thr Phe Pro Val Asn Val Ala Phe Leu
165 170 175

Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Met Asp Glu Glu
180 185 190

Ile Gly Pro Phe Glu Ser Thr Ser Val Ala Gln Ala Val His Asn Cys
195 200 205

Gly Gly Lys Val Val Val Gln Val Lys Asp Val Val Ala His Gly Ser
210 215 220

Leu Asp Pro Arg Met Val Lys Ile Pro Gly Ile Tyr Val Asp Tyr Val
225 230 235 240

Val Val Ala Ala Pro Glu Asp His Gln Gln Thr Tyr Asp Cys Glu Tyr
245 250 255

Asp Pro Ser Leu Ser Gly Glu His Arg Ala Pro Glu Gly Ala Thr Asp
260 265 270

Ala Ala Leu Pro Met Ser Ala Lys Lys Ile Ile Gly Arg Arg Gly Ala
275 280 285

Leu Glu Leu Thr Glu Asn Ala Val Val Asn Leu Gly Val Gly Ala Pro
290 295 300

Glu Tyr Val Ala Ser Val Ala Gly Glu Glu Gly Ile Ala Asp Thr Ile
305 310 315 320

Thr Leu Thr Val Glu Gly Gly Ala Ile Gly Gly Val Pro Gln Gly Gly
325 330 335

Ala Arg Phe Gly Ser Ser Arg Asn Ala Asp Ala Ile Ile Asp His Thr
340 345 350

Tyr Gln Phe Asp Phe Tyr Asp Gly Gly Gly Leu Asp Ile Ala Tyr Leu
355 360 365

Gly Leu Ala Gln Cys Asp Gly Ser Gly Asn Ile Asn Val Ser Lys Phe
370 375 380

Gly Thr Asn Val Ala Gly Cys Gly Gly Phe Pro Asn Ile Ser Gln Gln
385 390 395 400

Thr Pro Asn Val Tyr Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys
405 410 415

Ile Ala Val Glu Asp Gly Lys Val Lys Ile Leu Gln Glu Gly Lys Ala
420 425 430

Lys Lys Phe Ile Lys Ala Val Asp Gln Ile Thr Phe Asn Gly Ser Tyr
435 440 445

Ala Ala Arg Asn Gly Lys His Val Leu Tyr Ile Thr Glu Arg Cys Val
450 455 460

Phe Glu Leu Thr Lys Glu Gly Leu Lys Leu Ile Glu Val Ala Pro Gly
465 470 475 480

Ile Asp Ile Glu Lys Asp Ile Leu Ala His Met Asp Phe Lys Pro Ile
485 490 495

Ile Asp Asn Pro Lys Leu Met Asp Ala Arg Leu Phe Gln Asp Gly Pro
500 505 510

Met Gly Leu Lys Lys
515

<210> 26
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 26
caagctgggt ctgttcatgc tggatg

26

<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 27
aagcggttct cgcctcgta aacctga

27

<210> 28
<211> 416
<212> PRT
<213> Porphyromonas gingivalis

<400> 28

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
1 5 10 15

Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly
35 40 45

Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Phe Ala Gly Gln Lys Asp Ala
130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His
210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly
325 330 335

Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly
370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
405 410 415

<210> 29
<211> 1251
<212> DNA
<213> Porphyromonas gingivalis

<220>
<221> CDS
<222> (1)..(1251)
<223>

<400> 29
atg gca gaa agt cgt aga aag tat tat ttc cct gat gtc acc gat gag 48
Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
1 5 10 15

caa tgg tac gac tgg cat tgg cag gtc ctc aat cga att gag acg ctc 96
Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
20 25 30

gac cag ctg aaa aag tac gtt aca ctc acc gct gaa gaa gag gga 144
Asp Gln Leu Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly
35 40 45

gta aaa gaa tcg ccc aaa gta ctc cga atg gct atc aca cct tat tat 192
Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
50 55 60

ttg agt ttg ata gac ccc gag aat cct aat tgt ccg att cgt aaa caa 240
Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
65 70 75 80

gcc att cct act caa cag gaa ctg gta cgt gct cct gaa gat cag gta 288
Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
85 90 95

gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat 336
Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
100 105 110

cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg 384
Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
115 120 125

tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct 432
Tyr Cys Arg His Cys Thr Arg Arg Phe Ala Gly Gln Lys Asp Ala
130 135 140

tct tct cct tct gag cgc atc gat cga tgc att gac tat ata gcc aat Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn 145 150 155 160	480
aca ccg aca gtc cgc gat gtt ttg cta tcg gga ggc gat gcc ctc ctt Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu 165 170 175	528
gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile 180 185 190	576
cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctc Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu 195 200 205	624
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His 210 215 220	672
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu 225 230 235 240	720
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu 245 250 255	768
ggg aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val 260 265 270	816
atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr 275 280 285	864
tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr 290 295 300	912
ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr 305 310 315 320	960
tcg ggc tat gca gtt cct acc ttt gtg gta ggt gct ccg ggg ggt ggt Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly 325 330 335	1008
ggg aag ata cct gta acg ccg aac tat gtt gta tct cag tcc cca cga Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg 340 345 350	1056
cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu 355 360 365	1104
ccg gag aat tat cat gag gag tgc gat tgt gag gac tgt cga gcc ggt	1152

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly			
370	375	380	
aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct			1200
Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala			
385	390	395	400
atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac			1248
Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn			
405		410	415
tga			1251
<210> 30			
<211> 416			
<212> PRT			
<213> <i>Porphyromonas gingivalis</i>			
<400> 30			
Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu			
1	5	10	15
Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu			
20	25	30	
Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly			
35	40	45	
Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr			
50	55	60	
Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln			
65	70	75	80
Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val			
85	90	95	
Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His			
100	105	110	
Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met			
115	120	125	
Tyr Cys Arg His Cys Thr Arg Arg Phe Ala Gly Gln Lys Asp Ala			
130	135	140	

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His
210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly
325 330 335

Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly

370

375

380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
405 410 415

<210> 31
<211> 471
<212> PRT
<213> *Bacillus subtilis*

<400> 31

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
1 5 10 15

Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
35 40 45

Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
85 90 95

His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp
100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
115 120 125

Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg
130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
325 330 335

Val Val Asp Ala Pro Gly Gly Lys Ile Ala Leu Gln Pro Asn
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
450 455 460

Glu Cys Gly Gly Asp Ser Ser
465 470

<210> 32
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 32
cgcattcaag tcaaagacgt tcaggcta 28

<210> 33
<211> 1387
<212> DNA
<213> Alcaligenes faecalis

<220>
<221> CDS
<222> (408)..(1304)
<223>

<400> 33
cattacacag gctctgcagc agtggcaggg cagtgccgac ccctgggtgt cccgtgccgc 60

gcaaaccttc gccaaagggtg cgcctggttc ggctcggttg tccttgagc tgctggagag 120

ggtgcatcac ctgtctttgg ccgatgtttt ccgtctggaa tacattgtgt cgctgcaatg 180

tggcgtacag ggcgacttcc aggaaggcat acgggcactg ctgattgata aagacaaaca 240

gccgcgctgg aatcctgcct cgctggaaaca ggcggatgca cgctgggtgg aacgttttt 300

tgttcctgcc	tggccggcag	aaacgactca	tcccttggct	gacctgtaac	ccaggcagac	360
cgctgcggcg	ccagacggcg	ccgcttcat	aatgacgagg	agacaaa	atg agt aac	416
					Met Ser Asn	
					1	
acg att gca ttt atc ggg ctg ggc cat atg ggt aaa ccc atg gcg ctg	5	10	15			464
Thr Ile Ala Phe Ile Gly Leu Gly His Met Gly Lys Pro Met Ala Leu						
aat ctg ctc aaa gcc ggt cat agc ctg aac gtc ttt gac ttg aat gcg	20	25	30	35		512
Asn Leu Leu Lys Ala Gly His Ser Leu Asn Val Phe Asp Leu Asn Ala						
caa gcc atg cag gaa ctg cag gca gca ggg gca cag gtg ggg gaa tcg	40	45	50			560
Gln Ala Met Gln Glu Leu Gln Ala Ala Gly Ala Gln Val Gly Glu Ser						
gcg gtg caa atc gcc caa gac gcg cag atg gtc ttt acc atg ctg cct	55	60	65			608
Ala Val Gln Ile Ala Gln Asp Ala Gln Met Val Phe Thr Met Leu Pro						
gct ggc cgc cat gtt cgt cag gtt tac gag ggc gag aac ggc ttg ctg	70	75	80			656
Ala Gly Arg His Val Arg Gln Val Tyr Glu Gly Glu Asn Gly Leu Leu						
cag act gtg gcc ccc ggt acg gtg ctg gtc gat tgc agc acc att gat	85	90	95			704
Gln Thr Val Ala Pro Gly Thr Val Leu Val Asp Cys Ser Thr Ile Asp						
gcg caa acc agc cag gat ctg gcg gcc aaa gcc agc aag ctg ggt ctg	100	105	110	115		752
Ala Gln Thr Ser Gln Asp Leu Ala Ala Lys Ala Ser Lys Leu Gly Leu						
ttc atg ctg gat gcg ccg gtc tcc ggt ggg acc ggt ggc gcc att gct	120	125	130			800
Phe Met Leu Asp Ala Pro Val Ser Gly Gly Thr Gly Gly Ala Ile Ala						
ggc acc ttg acc ttt atg gtc ggg ggc gag gat cag gcc ctg gaa aag	135	140	145			848
Gly Thr Leu Thr Phe Met Val Gly Gly Glu Asp Gln Ala Leu Glu Lys						
gcg cgc cct tac ttg gat gcc atg ggc aag aac att ttc cac gcg ggt	150	155	160			896
Ala Arg Pro Tyr Leu Asp Ala Met Gly Lys Asn Ile Phe His Ala Gly						
aaa gcc ggt gcg ggt cag gtt gcc aag att tgc aac aat atg ctc ttg	165	170	175			944
Lys Ala Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn Met Leu Leu						
ggg att ttg atg gcg ggt act gct gaa gcc ttg gct ttg ggc gtt gcc	180	185	190	195		992
Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu Gly Val Ala						
cac ggt ctg gac cct gcc gtg ctg tcg acc atc atg gcg cgc agt tcc						1040
His Gly Leu Asp Pro Ala Val Leu Ser Thr Ile Met Ala Arg Ser Ser						

200

205

210

ggt cga aac tgg gca acc gag ctg tac aac ccc tgg cct ggg gtg atg 1088
 Gly Arg Asn Trp Ala Thr Glu Leu Tyr Asn Pro Trp Pro Gly Val Met
 215 220 225

ccg gat gta ccg gct tcg cgt gat tat cag ggc ggt ttt gcg acg ggc 1136
 Pro Asp Val Pro Ala Ser Arg Asp Tyr Gln Gly Phe Ala Thr Gly
 230 235 240

ctg atg ctc aaa gac ctg ggt ctg gca gcc gat gcg gct gtc agc cag 1184
 Leu Met Leu Lys Asp Leu Gly Leu Ala Ala Asp Ala Ala Val Ser Gln
 245 250 255

aac agc gcg acg cct ttg ggc gaa ctg gca cgt aac ctg ttc gcc ttg 1232
 Asn Ser Ala Thr Pro Leu Gly Glu Leu Ala Arg Asn Leu Phe Ala Leu
 260 265 270 275

cac gcc gca caa ggt cag aat gca ggg ctg gat ttc tcc agc att ctt 1280
 His Ala Ala Gln Gly Gln Asn Ala Gly Leu Asp Phe Ser Ser Ile Leu
 280 285 290

aat ttg tac cgt cag aag cac taa gttctggcag tgcgttagggc aggggctgca 1334
 Asn Leu Tyr Arg Gln Lys His
 295

gttccagcgc ctgtccttgc tccaaattgaa actggccttg ttccaggtcc gcc 1387

<210> 34
 <211> 298
 <212> PRT
 <213> Alcaligenes faecalis

<400> 34

Met Ser Asn Thr Ile Ala Phe Ile Gly Leu Gly His Met Gly Lys Pro
 1 5 10 15

Met Ala Leu Asn Leu Leu Lys Ala Gly His Ser Leu Asn Val Phe Asp
 20 25 30

Leu Asn Ala Gln Ala Met Gln Glu Leu Gln Ala Ala Gly Ala Gln Val
 35 40 45

Gly Glu Ser Ala Val Gln Ile Ala Gln Asp Ala Gln Met Val Phe Thr
 50 55 60

Met Leu Pro Ala Gly Arg His Val Arg Gln Val Tyr Glu Gly Glu Asn
 65 70 75 80

Gly Leu Leu Gln Thr Val Ala Pro Gly Thr Val Leu Val Asp Cys Ser

Thr Ile Asp Ala Gln Thr Ser Gln Asp Leu Ala Ala Lys Ala Ser Lys
100 105 110

Leu Gly Leu Phe Met Leu Asp Ala Pro Val Ser Gly Gly Thr Gly Gly
115 120 125

Ala Ile Ala Gly Thr Leu Thr Phe Met Val Gly Gly Glu Asp Gln Ala
130 135 140

Leu Glu Lys Ala Arg Pro Tyr Leu Asp Ala Met Gly Lys Asn Ile Phe
145 150 155 160

His Ala Gly Lys Ala Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn
165 170 175

Met Leu Leu Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu
180 185 190

Gly Val Ala His Gly Leu Asp Pro Ala Val Leu Ser Thr Ile Met Ala
195 200 205

Arg Ser Ser Gly Arg Asn Trp Ala Thr Glu Leu Tyr Asn Pro Trp Pro
210 215 220

Gly Val Met Pro Asp Val Pro Ala Ser Arg Asp Tyr Gln Gly Gly Phe
225 230 235 240

Ala Thr Gly Leu Met Leu Lys Asp Leu Gly Leu Ala Ala Asp Ala Ala
245 250 255

Val Ser Gln Asn Ser Ala Thr Pro Leu Gly Glu Leu Ala Arg Asn Leu
260 265 270

Phe Ala Leu His Ala Ala Gln Gly Gln Asn Ala Gly Leu Asp Phe Ser
275 280 285

Ser Ile Leu Asn Leu Tyr Arg Gln Lys His
290 295

<210> 35
<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 35
gggaattcca tatggtaggt aaaaaggttg tacatc 36

<210> 36
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 36
cgacggatcc attcgccgc ttgaataact aaag 34

<210> 37
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 37
cgacggatcc cgaaaatgtc accaaaaatt attgag 36

<210> 38
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 38
agagagcata tgtctttca cttcgcc 28

<210> 39
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 39
agagaggat ccgcggctcc cacaatgtt aatg 35

<210> 40
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 40
agagagcata tgacaaataa tgaaagcaaa gg 32

<210> 41
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 41
gggaattcca tatgagaaaa gtagaaatca ttacagctg 39

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acggtgatct cttctacat tatttttca gtcccatg 38

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catgggactg aaaaaataat gtagaaggag atcaacgt 38

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cgacggatcc tcaacgacca ctgaagttgg 30

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ctagtctaga gctttctaag aaacgatttc cg 32

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ctagtctaga ggaaaccgct taacgaactc 30

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ccggaattct ttaatatgcg atttggagga g 31

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Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp

1

5

10

15

gct cac tat act gga aac tta gta aac ggc gct aga atc gtg aat cag 96
 Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln
 20 25 30

tgg ggc gac gta ggt aca gaa tta atg gtt tat gtt gat ggt gac atc 144
 Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
 35 40 45

agc tta ttc ttg ggc tac aaa gat atc gaa ttc aca gct cct gta tat 192
 Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr
 50 55 60

gtt ggt gat ttt atg gaa tac cac ggc tgg att gaa aaa gtt ggc aac 240
 Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn
 65 70 75 80

cag tcc tat aca tgt aaa ttt gaa gca tgg aaa gta gca aag atg gtt 288
 Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Lys Met Val
 85 90 95

gat atc aca aat cca cag gat aca cgt gca aca gct tgt gaa cct ccg 336
 Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro
 100 105 110

gta ctt tgt ggt act gca aca ggc agc ctt ttc atc gca aag gat aat 384
 Val Leu Cys Gly Thr Ala Thr Gly Ser Leu Phe Ile Ala Lys Asp Asn
 115 120 125

cag aga ggt cct cag gaa tct tcc ttc aag gat gca aag cac cct caa 432
 Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Asp Ala Lys His Pro Gln
 130 135 140

taa 435

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Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp
 1 5 10 15

Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln
 20 25 30

Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
 35 40 45

Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr

50

55

60

Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn
65 70 75 80

Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Lys Met Val
85 90 95

Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro
100 105 110

Val Leu Cys Gly Thr Ala Thr Gly Ser Leu Phe Ile Ala Lys Asp Asn
115 120 125

Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Asp Ala Lys His Pro Gln
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43

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<211> 30

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<213> Artificial Sequence

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<223> PCR primer

<400> 56

ctagtctaga tcaacgacca ctgaaggttgg

30

<210> 57

<211> 40

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40

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ggaggggatt cttcatgaag taaggaggag atcttatatg gttgactttg agtttgatta	60	
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gactagatat ctcaggagta ctcatgggtg aa 32